

SEQUENCE LISTING

RECEIVED

JUL 3 2002

<110> Willson, Tracy
 Nicola, Nicos A.
 Hilton, Douglas J.
 Metcalf, Donald
 Zhang, Jian G.

TECH CENTER 1600/2900

- <120> NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES ENCODING SAME
- <130> Davies Collison Cave
- <140> 09/688,286
- <141> 2000-10-13
- <150> 09/051,843
- <151> 1998-06-29
- <160> 11
- <170> PatentIn Ver. 2.0
- <210> 1
- <211> 1383
- <212> DNA
- <213> Unknown Organism
- <220>
- <220>
- <221> CDS
- <222> (61)..(1338)
- <220>
- <221> unsure
- <222> (121)
- <223> n=authors are unsure of exact sequence in this region
- <220>
- <221> unsure
- <222> (122)
- <223> n=authors are unsure of exact sequence in this

<222	2> (: 3> n:		nors	are	unsı	ure (of e	xact	seqi	uence	e in	this	5			
<222	l> u1 2> (0 3> n:		nors	are	unsı	ure (of e:	xact	seqi	uence	e in	this	5			
<222	l> u1 2> (6 3> n=		nors	are	unsı	ıre (of e:	xact	seqi	uence	e in	this	5			
<220					ē											
	L> u: 2> (6	nsure 642)	9													
	3> n=			are	unsı	ire (o√f e:	xact	sequ	uence	e in	this	5			
<400)> 1						1									
tgaa	aaaga	ata g	gaata	aaat	gg co	ctcgi	tgcc	g aat	ttcg	gcac	gago	ccga	ggc g	gaggg	gcctgc	60
					.*	,										
										ttg Leu						108
										gcc Ala					cca Pro	156
										aat Asn						204
										cca Pro						252
		_			_	_		_	_	aag Lys			_		_	300

		_			_			_	_				_	ctg Leu 95	_	348
														cct Pro		396
		_	_					_		_				gct Ala		444
			_	_					_	_		_	_	tgt Cys		492
														ctg Leu		540
			_	_	_			_	_		_			atc Ile 175		588
_	-					_	-				_			gtg Val	_	636
														gat Asp		684
_						Ser	Cys	Lys		Val				tcc Ser		732
			_											aat Asn		780
_				_		_						_	_	aga Arg 255	_	828
			-			_						_	_	cat His		876

.

-)-

														gat Asp		924
	_				_	_						_		gcc Ala		972
														tgc Cys		1020
_	-			_		_	_		_	_	_	_	_	ata Ile 335		1068
_										_				att Ile		1116
_		_	_		_	_							_	aaa Lys		1164
	_									_			_	att Ile		1212
		_			_	_		_	_		_			aag Lys	_	1260
	_								_	_	_	_		gta Val 415		1308
	ata Ile									tgat	gggg	gag a	aagto	gattt	EC .	1358
tttc	ettge	cct t	caat	gtga	ac co	ctgt										1383

<210> 2 <211> 426

- -4

<213> Unknown Organism

<220>

<220>

<221> unsure

<222> (21)

<223> authors are unsure about the sequence assignment

<220>

<221> unsure

<222> (194)

<223> authors are unsure about the sequence assignment

<400> 2

Met Ala Arg Pro Ala Leu Leu Glý Glu Leu Leu Val Leu Leu Leu Trp
1 5 10 15

Thr Ala Thr Val Xaa Gly Gln Val Ala Ala Ala Thr Glu Val Gln Pro
20 25 30

Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Ile Ile 35 40 45

Trp Thr Trp Ser Pro Pro Glu Gly Ala Ser Pro Asn Cys Thr Leu Arg
50 55 60

Tyr Phe Ser His Phe Asp Asp Gln Gln Asp Lys Lys Ile Ala Pro Glu 65 70 75 80

Thr His Arg Lys Glu Glu Leu Pro Leu Asp Glu Lys Ile Cys Leu Gln
85 90 95

Val Gly Ser Gln Cys Ser Ala Asn Glu Ser Glu Lys Pro Ser Pro Leu 100 105 110

Val Lys Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val 115 120 125

Thr Glu Leu Lys Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser 130 135 140

Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr His Tyr Thr Leu Tyr

Tyr Trp Tyr Ser Ser Leu Glu Lys Ser Arg Gln Cys Glu Asn Ile Tyr Arg Glu Gly Gln His Ile Ala Cys Ser Phe Lys Leu Thr Lys Val Glu Pro Xaa Ser Phe Glu His Gln Asn Val Gln Ile Met Val Lys Asp Asn Ala Gly Lys Ile Arg Pro Ser Cys Lys Ile Val Ser Leu Thr Ser Tyr Val Lys Pro Asp Pro Pro His Ile Lys His Leu Leu Leu Lys Asn Gly Ala Leu Leu Val Gln Trp Lys Asn Pro Gln Asn Phe Arg Ser Arg Cys Leu Thr Tyr Glu Val Glu Val Asn Asn Thr Gln Thr Asp Arq His Asn Ile Leu Glu Val Glu Glu Asp Lys Cys Gln Asn Ser Glu Ser Asp Arq Asn Met Glu Gly Thr Ser Cys Phe Gln Leu Pro Gly Val Leu Ala Asp Ala Val Tyr Thr Val Arq Val Arq Val Lys Thr Asn Lys Leu Cys Phe Asp Asp Asn Lys Leu Trp Ser Asp Trp Ser Glu Ala Gln Ser Ile Gly Lys Glu Gln Asn Ser Thr Phe Tyr Thr Thr Met Leu Leu Thr Ile Pro Val Phe Val Ala Val Ala Val Ile Ile Leu Leu Phe Tyr Leu Lys Arg Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys Tyr Asp Ile Tyr Glu Lys Gln Ser Lys Glu Glu Thr Asp Ser Val Val

Leu Ile Glu Asn Leu Lys Lys Ala Ala Pro 420 425

<210> 3 <211> 1383 <212> DNA <213> Unknown Organism														
<220> <223> Description of Unknown Organism:Human IL-13 receptor alpha-chain														
<220> <221> CDS <222> (61)(1338)														
<400> 3 gagtctaaca cggaccaagg agtttaacac gtgcggccgg gttccgaggc gagaggctgc 60														
atg gag tgg ccg gcg ctc tgc ggg ctg tgg gcg ctg ct														
gcc ggc ggc ggg ggc ggg ggc gcg cct acg gaa act cag cca 156 Ala Gly Gly Gly Gly Gly Gly Gly Ala Pro Thr Glu Thr Gln Pro 20 25 30														
cct gtg aca aat ttg agt gtc tct gtt gaa aac ctc tgc aca gta ata 204 Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Val Ile 35 40 45														
tgg aca tgg aat cca ccc gag gga gcc agc tca aat tgt agt cta tgg 252 Trp Thr Trp Asn Pro Pro Glu Gly Ala Ser Ser Asn Cys Ser Leu Trp 50 55 60														
tat ttt agt cat ttt ggc gac aaa caa gat aag aaa ata gct ccg gaa 300 Tyr Phe Ser His Phe Gly Asp Lys Gln Asp Lys Lys Ile Ala Pro Glu 65 70 75 80														
act cgt cgt tca ata gaa gta ccc ctg aat gag agg att tgt ctg caa 348 Thr Arg Arg Ser Ile Glu Val Pro Leu Asn Glu Arg Ile Cys Leu Gln 85 90 95														
gtg ggg tcc cag tgt agc acc aat gag agt gag aag cct agc att ttg 396 Val Gly Ser Gln Cys Ser Thr Asn Glu Ser Glu Lys Pro Ser Ile Leu 100 105 110														

_	gaa Glu		_					_		_				_		444
	gag Glu 130			_					_	_		_	_	_		492
	ctc Leu															540
	tgg Trp		_			_					_	_				588
_	gaa Glu						-			_	_				_	636
_	tcc Ser	_		_				_			_	_	_	_		684
_	gga Gly 210															732
	aaa Lys		_												-	780
_	cta Leu								_				_	_	_	828
	ttt Phe		-	_	_	_			_							876
	ttc Phe															924
	gtg Val 290					_		_	_			_			-	972

.

act ttg aac aca gtc aga ata aga gtc aaa aca aat aag tta tgc tat Thr Leu Asn Thr Val Arg Ile Arg Val Lys Thr Asn Lys Leu Cys Tyr 305 310 320	1020
gag gat gac aaa ctc tgg agt aat tgg agc caa gaa atg agt ata ggt Glu Asp Asp Lys Leu Trp Ser Asn Trp Ser Gln Glu Met Ser Ile Gly 325	1068
aag aag cgc aat tcc aca ctc tac ata acc atg tta ctc att gtt cca Lys Lys Arg Asn Ser Thr Leu Tyr Ile Thr Met Leu Leu Ile Val Pro 340 345 350	1116
gtc atc gtc gca ggt gca atc ata gta ctc ctg ctt tac cta aaa agg Val Ile Val Ala Gly Ala Ile Ile Val Leu Leu Tyr Leu Lys Arg 355 360 365	1164
ctc aag att att ata ttc cct cca att cct gat cct ggc aag att ttt Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe 370 375 380	1212
aaa gaa atg ttt gga gac cag aat gat gat act ctg cac tgg aag aag Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys 385 390 395 400	1260
tac gac atc tat gag aag caa acc aag gag gaa acc gac tct gta gtg Tyr Asp Ile Tyr Glu Lys Gln Thr Lys Glu Glu Thr Asp Ser Val Val 405 410 415	1308
ctg ata gaa aac ctg aag aaa gcc tct cag tgatggagat aatttattt Leu Ile Glu Asn Leu Lys Lys Ala Ser Gln 420 425	1358
taccttcact gtgaccttga gaaga	1383

<210> 4

<211> 426

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Human IL-13 receptor alpha-chain

<400> 4

_ \ /

Met Glu Trp Pro Ala Arg Leu Cys Gly Leu Trp Ala Leu Leu Cys

1 5 10 15

Ala Gly Gly Gly Gly Gly Gly Ala Pro Thr Glu Thr Gln Pro
20 25 30

Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Val Ile 35 40 45

Trp Thr Trp Asn Pro Pro Glu Gly Ala Ser Ser Asn Cys Ser Leu Trp 50 55 60

Tyr Phe Ser His Phe Gly Asp Lys Gln Asp Lys Lys Ile Ala Pro Glu 65 70 75 80

1

Thr Arg Arg Ser Ile Glu Val Pro Leu Asm Glu Arg Ile Cys Leu Gln 85 90 95

Val Gly Ser Gln Cys Ser Thr Asn Glu Ser Glu Lys Pro Ser Ile Leu 100 105 110

Val Glu Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val 115 120 125

Thr Glu Leu Gln Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser 130 135 140

Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr Asn Tyr Thr Leu Tyr 145 150 155 160

Tyr Trp His Arg Ser Leu Glu Lys Ile His Gln Cys Glu Asn Ile Phe 165 170 175

Arg Glu Gly Gln Tyr Phe Gly Cys Ser Phe Asp Leu Thr Lys Val Lys 180 185 190

Asp Ser Ser Phe Glu Gln His Ser Val Gln Ile Met Val Lys Asp Asn 195 200 205

Ala Gly Lys Ile Lys Pro Ser Phe Asn Ile Val Pro Leu Thr Ser Arg 210 215 220

Val Lys Pro Asp Pro Pro His Ile Lys Asn Leu Ser Phe His Asn Asp 225 230 235 240

Asp Leu Tyr Val Gln Trp Glu Asn Pro Gln Asn Phe Ile Ser Arg Cys

Leu Phe Tyr Glu Val Glu Val Asn Asn Ser Gln Thr Glu Thr His Asn 260 265 270

Val Phe Tyr Val Gln Glu Ala Lys Cys Glu Asn Pro Glu Phe Glu Arg 275 280 285

Asn Val Glu Asn Thr Ser Cys Phe Met Val Pro Gly Val Leu Pro Asp 290 295 300

Thr Leu Asn Thr Val Arg Ile Arg Val Lys Thr Asn Lys Leu Cys Tyr 305 310 315 320

Glu Asp Asp Lys Leu Trp Ser Asn Trp Ser Gln Glu Met Ser Ile Gly 325 330 335

Lys Lys Arg Asn Ser Thr Leu Tyr Ile Thr Met Leu Leu Ile Val Pro 340 345 350

Val Ile Val Ala Gly Ala Ile Ile Val Leu Leu Tyr Leu Lys Arg 355 360 365

Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe 370 375 380

Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys 385 390 395 400

Tyr Asp Ile Tyr Glu Lys Gln Thr Lys Glu Glu Thr Asp Ser Val Val
405 410 415

Leu Ile Glu Asn Leu Lys Lys Ala Ser Gln
420 425

<210> 5

11

<211> 30

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: signal sequence of murine IL-3

<400>5

Met Val Leu Ala Ser Ser Thr Thr Ser Ile His Thr Met Leu Leu 1 5 10 15

Leu Leu Met Leu Phe His Leu Gly Leu Gln Ala Ser Ile Ser 20 <210> 6 <211> 8 <212> PRT <213> Unknown Organism <220> <223> Description of Unknown Organism: N-terminal FLAG epitope-tag <400> 6 Asp Tyr Lys Asp Asp Asp Lys <210> 7 <211> 31 <212> DNA <213> Artificial Sequence <220> <223> Description of Artificial Sequence:Oligo 1478 5' <400> 7 agcttctaga acagaagttc agccacctgt g 31 <210> 8 <211> 30 <212> DNA <213> Artificial Sequence <220> <223> Description of Artificial Sequence:Oligo 1480 5' <400> 8 aactccacct tctacaccac ctgatctaga 30 <210> 9

```
<211> 5
<212> PRT
<213> Unknown Organism
<220>
<223> Description of Unknown Organism: NR4 Motif
<220>
<221> Unsure
<222> (3)
<223> Xaa may be any amino acid
<400> 9
Trp Ser Xaa Trp Ser
  1
<210> 10
<211> 27
<212> PRT
<213> Unknown Organism
<220>
<223> Description of Unknown Organism: N-term amino acid sequence
      of mNR4 (major)
<220>
<221> Unsure
<222> (24)
<223> Xaa may be any amino acid
<400> 10
Asp Tyr Lys Asp Asp Asp Asp Tyr Lys Asp Asp Glu Ser Arg Thr Glu
Val Gln Pro Pro Val Thr Xaa Leu Ser Val
         20
<210> 11
<211> 27
<212> PRT
<213> Unknown Organism
<220>
<223> Description of Unknown Organism: N-term amino acid sequence of
      mNR4 (minor)
```

1

Val Gln Pro Pro Val Thr Xaa Leu Ser Val

1 · 1